Table e: Clinical features of 52 patients with KCNQ2-related disorder

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Patient | Gender | Age at onset (day) | Follow-up time (months) | Development | Variants | Location | Type of variants | GnomAD/1000gnome | Clinvar/HGMD | Reference | Familial targeted variantion study |
| 1 | M | 2 | 26 | C | NM\_172107:exon15:c.1632T>G(p.C544W) | C-terminal region | missense | 0/0 | / | / | De novo |
| 2 | M | 2 | 28 | C | NM\_172107:exon8:c.1064A>T(p.D355V) | C-terminal region | missense | 0/0 | / | / | De novo |
| 3 | F | 10 | 26 | C | NM\_172107:exon1:c.205del(p.K69Qfs\*51) | N-terminal region | frameshift | 0/0 | Pathogenic/DM | PMID 14985406 | / |
| 4 | M | 13 | 21 | D | NM\_172107:exon4:c.638G>A(p.R213Q) | voltage-sensor  helix /S4 | missense | 0/0 | Pathogenic/DM | PMID 22275249 | / |
| 5 | F | 4 | 25 | B | NM\_172107:exon14:c.1609A>T(p.K537X) | C-terminal region | stop\_gained | 0/0 | Pathogenic/DM | PMID 24375629 | / |
| 6 | M | 4 | 16 | A | NM\_172107:exon4:c.553G>A(p.A185T) | S3 | missense | 0/0 | / | / | De novo |
| 7 | M | 13 | 30 | C | NM\_172107:exon15:c.1657C>T(p.R553W) | C-terminal region | missense | 0/0 | Pathogenic/DM | PMID 23621294 | / |
| 8 | F | 1 | 12 | A | NM\_172107:exon17:c.2127del(p.V710Cfs\*155) | C-terminal region | frameshift | 0/0 | Pathogenic/DM | PMID 29655203 | / |
| 9 | F | 3 | 39 | A | NM\_172107:exon13:c.1342C>T(p.R448X) | C-terminal region | stop\_gained | 0/0 | Pathogenic/DM | PMID 11690625 | / |
| 10 | F | 2 | 18 | D | NM\_172107:exon4:c.638G>A(p.R213Q) | S4 | missense | 0/0 | Pathogenic/DM | PMID 22275249 | De novo |
| 11 | F | 4 | 24 | A | NM\_172107:exon14:c.1631+1G>A | C-terminal region | splice\_region | 0/0 | Pathogenic/DM | PMID 25982755 | / |
| 12 | F | 3 | 40 | A | NM\_172107:exon14:c.1601del(p.P534Rfs\*31) | C-terminal region | frameshift | 0/0 | Likely Benign/NA | / | / |
| 13 | F | 3 | 39 | B | NM\_172107:exon8:c.1040A>G(p.Y347C) | C-terminal region | missense | 0/0 | / | / | / |
| 14 | F | 3 | 50 | A | NM\_172107:exon13:c.1452G>A(p.W484X) | C-terminal region | stop\_gained | 0/0 | / | / | De novo |
| 15 | F | 4 | 30 | A | NM\_172107:exon8:c.1027G>T(p.A343S) | C-terminal region | missense | 0/0 | / | / | / |
| 16 | F | 1 | 18 | A | NM\_172107:exon2:c.365C>T(p.S122L) | the extracellular domain between the S1 segment and the S2 segment | missense | 0/0 | Pathogenic/DM | PMID 16916607 | / |
| 17 | F | 7 | 38 | A | NM\_172107:exon11:c.1230del(p.P411Rfs\*29) | C-terminal region | frameshift | 0/0 | NA/DM | / | Paternal |
| 18 | M | 9 | 12 | A | NM\_172107:exon4:c.668C>T(p.S223F) | Cytoplasmic between S4 segment and S5 segment | missense | 0/0 | / | / | / |
| 19 | F | 3 | 13 | A | NM\_172107:exon4:c.620G>A(p.R207Q) | S4 | missense | 0/0 | Pathogenic/DM | PMID 17872363 | De novo |
| 20 | M | 3 | 16 | A | NM\_172107:exon1:c.242T>C(p.L81P) | N | missense | 0/0 | NA/DM | PMID 29215089 | / |
| 21 | M | 3 | 42 | A | NM\_172107:exon5:c.816+1G>A | Pore loop/H5 | splice\_region | 0/0 | Likely pathogenic/NA | / | / |
| 22 | M | 2 | 14 | D | NM\_172107:exon5:c.794C>T(p.A265V) | H5 | missense | 0/0 | Pathogenic/DM | PMID 22926866 | / |
| 23 | F | 1 | 15 | D | NM\_172107:exon5:c.796G>C(p.D266H) | H5 | missense | 0/0 | / | / | / |
| 24 | M | 2 | 5(deceased) | D | NM\_172107:exon5:c.793G>A(p.A265T) | H5 | missense | 0/0 | Pathogenic/DM | PMID 23692823 | / |
| 25 | M | 12 | 16 | D | NM\_172107:exon4:c.617T>G(p.L206R) | S4 | missense | 0/0 | / | / | De novo |
| 26 | M | 4 | 49 | B | NM\_172107:exon4:c.587C>T(p.A196V) | S4 | missense | 0/0 | Pathogenic/DM | PMID 17475800 | De novo |
| 27 | M | 2 | 36 | C | NM\_172107:exon4:c.637C>T(p.R213W) | S4 | missense | 0/0 | Pathogenic/DM | PMID 18353052 | / |
| 28 | M | 2 | 7 (deceased) | D | NM\_172107:exon4:c.629G>A(p.R210H) | S4 | missense | 0/0 | Pathogenic/DM | PMID 24107868 | / |
| 29 | F | 4 | 28 | D | NM\_172107:exon4:c.632T>G(p.M211R) | S4 | missense | 0/0 | / | / | De novo |
| 30 | F | 2 | 24 | A | NM\_172107:exon7:c.997C>T(p.R333W) | C-terminal region | missense | 0/0 | NA/DM | PMID 16039833 | / |
| 31 | M | 13 | 24 | D | NM\_172107:exon5:c.715G>C(p.G239R) | Pore domain/S5 | missense | 0/0 | Pathogenic/DM | PMID 23692823 | De novo |
| 32 | M | 1 | 12 | C | NM\_172107:exon5:c.749T>G(p.V250G) | S5 | missense | 0/0 | Pathogenic/DM | PMID 11690625 | De novo |
| 33 | M | 3 | 14 | C | NM\_172107:exon5:c.794C>T(p.A265V) | H5 | missense | 0/0 | Pathogenic/DM | PMID 22926866 | De novo |
| 34 | M | 24 | 12 | D | NM\_172107:exon4:c.568A>T(p.N190Y) | the extracellular domains between the S3 segment and the S4 segment | missense | 0/0 | / | / | / |
| 35 | F | 1 | 52 | D | NM\_172107:exon5:c.781T>A(p.F261I) | Pore loop | missense | 0/0 | / | / | De novo |
| 36 | F | 3 | 14 | D | NM\_172107:exon15:c.1678C>T(p.R560W) | C-terminal region | missense | 0/0 | Pathogenic/DM | PMID 22275249 | / |
| 37 | F | 2 | 25 | C | NM\_172107:exon15:c.1678C>T(p.R560W) | C-terminal region | missense | 0/0 | Pathogenic/DM | PMID 22275249 | / |
| 38 | F | 3 | 22 | D | NM\_172107:exon15:c.1687G>A(p.D563N) | C-terminal region | missense | 0/0 | Pathogenic/DM | PMID 26007637 | / |
| 39 | F | 1 | 40 | C | NM\_172107:exon17:c.2331del(p.E778Rfs\*152) | C-terminal region | frameshift | 0/0 | Likely benign-related/NA | / | De novo |
| 40 | M | 2 | 50 | D | NM\_172107:exon8:c.1049A>T(p.N350I) | C-terminal region | missense | 0/0 | Likely pathogenic/NA | / | De novo |
| 41 | M | 11 | 12 | C | NM\_172107:exon15:c.1687G>A(p.D563N) | C-terminal region | missense | 0/0 | Pathogenic/DM | PMID 26007637 | De novo |
| 42 | M | 3 | 12 | A | NM\_172107：exon3：c.484\_485delAA(p.K162Vfs\*10) | Cytoplasmic between S2 segment and S3 segment | frameshift | 0/0 | / | / | Paternal |
| 43 | M | 2 | 12 | C | NM\_172107：exon6：c.821C>T(p.T274M) | H5 | missense | 0/0 | Pathogenic /DM | PMID 22275249 | / |
| 44 | M | 1 | 16 | A | NM\_172107：exon4：c.650C>T(p.T217I) | S4 | missense | 0/0 | Likely pathogenic/NA | / | De novo |
| 45 | M | 2 | 12 | C | NM\_172107：exon5：c.807G>T(p.W269C) | H5 | missense | 0/0 | NA/DM-related | PMID 14534157 | De novo |
| 46 | F | 1 | 54 | C | NM\_172107：exon5: c.794C>T(p.A265V) | H5 | missense | 0/0 | Pathogenic/DM | PMID 22926866 | De novo |
| 47 | M | 7 | 37 | C | NM\_172107:exon5:c.715G>C(p.G239R) | S5 | missense | 0/0 | Pathogenic/DM | PMID 23692823 | De novo |
| 48 | F | 2 | 46 | C | NM\_172107:exon4:c.602G>A(p.R201H) | S4 | missense | 0/0 | Pathogenic/DM | PMID 23708187 | De novo |
| 49 | M | 2 | 63 | C | NM\_172107: exon4: c.637C>T(p.R213W) | S4 | missense | 0/0 | Pathogenic/DM | PMID 18353052 | De novo |
| 50 | M | 3 | 12 | C | NM\_172107:exon15:c.1678C>T(p.R560W) | C-terminal region | missense | 0/0 | Pathogenic/DM | PMID 22275249 | De novo |
| 51 | F | 1 | 24 | C | NM\_172107:exon5:c.740C>T(p.S247L) | Pore domain/S5 | missense | 0/0 | Pathogenic/Likely pathogenic​/DM-related | PMID 16916607 | De novo |
| 52 | M | 2 | 12 | C | NM\_172107：exon6：c.822\_831delinsC(p.L275\_T277del) | H5 | Microsatellite | 0/0 | NA/DM-related | / | De novo |

M=male; F=female; A= normal group; B= mild impairment group; C= encephalopathy group, including patients deceased; NA or /= no relevant information.